



Sequence List

<110> Betenbaugh et al.

<120> Engineering Intracellular Sialylation Pathways

<130> PF509P2

<140> 09/930,440

<141> 2001-08-16

<150> 60/227,579

<151> 2000-08-25

<150> 09/516,793

<151> 2000-03-01

<150> 60/169,624

<151> 1999-12-08

<150> 60/122,582

<151> 1999-03-02

<160> 8 ✓

<170> PatentIn Ver. 2.1

<210> 1

<211> 1429

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(693)

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acg cca atg act gag aat gga gaa atc aac ttt tca gta att ggt cag	96
Thr Pro Met Thr Glu Asn Gly Glu Ile Asn Phe Ser Val Ile Gly Gln	
20 25 30	

tat gtg gat tat ctt gtg aaa gaa cag gga gtg aag aac att ttt gtg	144
Tyr Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Val	
35 40 45	

aat ggc aca aca gga gaa ggc ctg tcc ctg agc gtc tca gag cgt cgc	192
Asn Gly Thr Thr Gly Glu Gly Leu Ser Leu Ser Val Ser Glu Arg Arg	
50 55 60	

cag gtt gca gag gag tgg gtg aca aaa ggg aag gac aag ctg gat cag	240
Gln Val Ala Glu Glu Trp Val Thr Lys Gly Lys Asp Lys Leu Asp Gln	
65 70 75 80	

gtg ata att cac gta gga gca ctg agc ttg aag gag tca cag gaa ctg	288
Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu	
85 90 95	

gcc caa cat gca gca gaa ata gga gct gat ggc atc gct gtc att gca 336
Ala Gln His Ala Ala Glu Ile Gly Ala Asp Gly Ile Ala Val Ile Ala
100 105 110

ccg ttc ttc ctc aag cca tgg acc aaa gat atc ctg att aat ttc cta 384
Pro Phe Phe Leu Lys Pro Trp Thr Lys Asp Ile Leu Ile Asn Phe Leu
115 120 125

aag gaa gtg gct gct gcc gcc cct gcc ctg cca ttt tat tac tat cac 432
Lys Glu Val Ala Ala Ala Pro Ala Leu Pro Phe Tyr Tyr Tyr His
130 135 140

att cct gcc ttg aca ggg gta aag att cgt gct gag gag ttg ttg gat 480
Ile Pro Ala Leu Thr Gly Val Lys Ile Arg Ala Glu Glu Leu Leu Asp
145 150 155 160

ggg att ctg gat aag atc ccc acc ttc caa ggg ctg aaa ttc agt gat 528
Gly Ile Leu Asp Lys Ile Pro Thr Phe Gln Gly Leu Lys Phe Ser Asp
165 170 175

aca gat ctc tta gac ttc ggg caa tgt gtt gat cag aat cgc cag caa 576
Thr Asp Leu Leu Asp Phe Gly Gln Cys Val Asp Gln Asn Arg Gln Gln
180 185 190

cag ttt gct ttc ctt ttt ggg gtg gat gag caa ctg ttg agt gct ctg 624
Gln Phe Ala Phe Leu Phe Gly Val Asp Glu Gln Leu Leu Ser Ala Leu
195 200 205

gtg atg gga gca act gga gca gtg ggc agt ttt gta tcc aga gat tta 672
Val Met Gly Ala Thr Gly Ala Val Gly Ser Phe Val Ser Arg Asp Leu
210 215 220

tca act ttg ttg tca aac tag gttttggagt gtcacagacc aaagccatca 723
Ser Thr Leu Leu Ser Asn
225 230

tgactctggg ctctgggatt ccaatgggcc caccctggct tccactgcag aaagcctcca 783

gggagtttac tgatagtgt gaagctaaac tgaagagcct ggatttcctt tctttcactg 843

atttaaagga tggaaacttg gaagctggta gctagtgcct ctctatcaaa tcagggtttg 903

caccttgaga cataatctac cttaaatagt gcattttttt ctcagggaat tttagatgaa 963

cttgaataaa ctctcctagc aaatgaaatc tcacaataag cattgaggta ccttttgtga 1023

gccttaaaaa gtcttatttt gtgaaggggc aaaaactcta ggagtcacaa ctctcagtca 1083

ttcatttcac agattttttt gtggagaaat ttctgtttat atggatgaaa tggaatcaag 1143

aggaaaattg taattgatta attccatctg tctttaggag ctctcattat ctcggtctct 1203

ggttcctaatt cctattttta agttgtctaa ttttaaacca ctataatatg tcttcatttt 1263

aataaatatt catttggaat ctaggaaaac tctgagctac tgcatttagg caggcacttt 1323

aataccaaac tgtaacatgt ctcaactgta tacaactcaa aatacaccag ctcatctggc 1383

tgctcagtct aactctagaa tggatgcttt tgaattcatt tcgatg 1429

<210> 2
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 <212> PRT
 <213> Homo sapiens

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 Thr Pro Met Thr Glu Asn Gly Glu Ile Asn Phe Ser Val Ile Gly Gln
 20 25 30
 Tyr Val Asp Tyr Leu Val Lys Glu Gln Gly Val Lys Asn Ile Phe Val
 35 40 45
 Asn Gly Thr Thr Gly Glu Gly Leu Ser Leu Ser Val Ser Glu Arg Arg
 50 55 60
 Gln Val Ala Glu Glu Trp Val Thr Lys Gly Lys Asp Lys Leu Asp Gln
 65 70 75 80
 Val Ile Ile His Val Gly Ala Leu Ser Leu Lys Glu Ser Gln Glu Leu
 85 90 95
 Ala Gln His Ala Ala Glu Ile Gly Ala Asp Gly Ile Ala Val Ile Ala
 100 105 110
 Pro Phe Phe Leu Lys Pro Trp Thr Lys Asp Ile Leu Ile Asn Phe Leu
 115 120 125
 Lys Glu Val Ala Ala Ala Ala Pro Ala Leu Pro Phe Tyr Tyr Tyr His
 130 135 140
 Ile Pro Ala Leu Thr Gly Val Lys Ile Arg Ala Glu Glu Leu Leu Asp
 145 150 155 160
 Gly Ile Leu Asp Lys Ile Pro Thr Phe Gln Gly Leu Lys Phe Ser Asp
 165 170 175
 Thr Asp Leu Leu Asp Phe Gly Gln Cys Val Asp Gln Asn Arg Gln Gln
 180 185 190
 Gln Phe Ala Phe Leu Phe Gly Val Asp Glu Gln Leu Leu Ser Ala Leu
 195 200 205
 Val Met Gly Ala Thr Gly Ala Val Gly Ser Phe Val Ser Arg Asp Leu
 210 215 220
 Ser Thr Leu Leu Ser Asn
 225 230

<210> 3
 <211> 1305
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1305)

<220>
 <221> misc_feature
 <222> (397)..(399)
 <223> The 'yat' at location 397..399 encodes amino acid His, or Tyr.

<220>
 <221> misc_feature
 <222> (406)..(408)
 <223> The 'gkt' at location 406..408 encodes amino acid Gly, or Val.

<220>
 <221> misc_feature
 <222> (439)..(441)
 <223> The 'yca' at location 439..441 encodes amino acid Pro, or Ser.

<220>
 <221> misc_feature
 <222> (505)..(507)
 <223> The 'gkt' at location 505..507 encodes amino acid Gly, or Val.

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 1 5 10 15
 ggg cga ccg tcc cgg ggc cgg ccg ccg aag ctg cag cgc aac tct cgc 96
 Gly Arg Pro Ser Arg Gly Arg Pro Pro Lys Leu Gln Arg Asn Ser Arg
 20 25 30
 ggc ggc cag ggc cga ggt gtg gag aag ccc ccg cac ctg gca gcc cta 144
 Gly Gly Gln Gly Arg Gly Val Glu Lys Pro Pro His Leu Ala Ala Leu
 35 40 45
 att ctg gcc cgg gga ggc agc aaa ggc atc ccc ctg aag aac att aag 192
 Ile Leu Ala Arg Gly Gly Ser Lys Gly Ile Pro Leu Lys Asn Ile Lys
 50 55 60
 cac ctg gcg ggg gtc ccg ctc att ggc tgg gtc ctg cgt gcg gcc ctg 240
 His Leu Ala Gly Val Pro Leu Ile Gly Trp Val Leu Arg Ala Ala Leu
 65 70 75 80
 gat tca ggg gcc ttc cag agt gta tgg gtt tcg aca gac cat gat gaa 288
 Asp Ser Gly Ala Phe Gln Ser Val Trp Val Ser Thr Asp His Asp Glu
 85 90 95
 att gag aat gtg gcc aaa caa ttt ggt gca caa gtt cat cga aga agt 336
 Ile Glu Asn Val Ala Lys Gln Phe Gly Ala Gln Val His Arg Arg Ser
 100 105 110
 tct gaa gtt tca aaa gac agc tct acc tca cta gat gcc atc ata gaa 384
 Ser Glu Val Ser Lys Asp Ser Ser Thr Ser Leu Asp Ala Ile Ile Glu
 115 120 125
 ttt ctt aat tat yat aat gag gkt gac att gta gga aat att caa gct 432
 Phe Leu Asn Tyr Xaa Asn Glu Xaa Asp Ile Val Gly Asn Ile Gln Ala
 130 135 140
 act tct yca tgt tta cat cct act gat ctt caa aaa gtt gca gaa atg 480
 Thr Ser Xaa Cys Leu His Pro Thr Asp Leu Gln Lys Val Ala Glu Met
 145 150 155 160
 att cga gaa gaa gga tat gat tct gkt ttc tct gtt gtg aga cgc cat 528
 Ile Arg Glu Glu Gly Tyr Asp Ser Xaa Phe Ser Val Val Arg Arg His
 165 170 175
 cag ttt cga tgg agt gaa att cag aaa gga gtt cgt gaa gtg acc gaa 576
 Gln Phe Arg Trp Ser Glu Ile Gln Lys Gly Val Arg Glu Val Thr Glu
 180 185 190
 cct ctg aat tta aat cca gct aaa cgg cct cgt cga caa gac tgg gat 624

Pro	Leu	Asn	Leu	Asn	Pro	Ala	Lys	Arg	Pro	Arg	Arg	Gln	Asp	Trp	Asp	
		195					200					205				
gga	gaa	tta	tat	gaa	aat	ggc	tca	ttt	tat	ttt	gct	aaa	aga	cat	ttg	672
Gly	Glu	Leu	Tyr	Glu	Asn	Gly	Ser	Phe	Tyr	Phe	Ala	Lys	Arg	His	Leu	
	210					215					220					
ata	gag	atg	ggg	tac	ttg	cag	ggg	gga	aaa	tgg	cat	act	acg	aaa	tgc	720
Ile	Glu	Met	Gly	Tyr	Leu	Gln	Gly	Gly	Lys	Trp	His	Thr	Thr	Lys	Cys	
	225				230					235					240	
gag	ctg	gaa	cat	agt	gtg	gat	ata	gat	gtg	gat	att	gat	tgg	cct	att	768
Glu	Leu	Glu	His	Ser	Val	Asp	Ile	Asp	Val	Asp	Ile	Asp	Trp	Pro	Ile	
				245				250						255		
gca	gag	caa	aga	gta	tta	aga	tat	ggc	tat	ttt	ggc	aaa	gag	aag	ctt	816
Ala	Glu	Gln	Arg	Val	Leu	Arg	Tyr	Gly	Tyr	Phe	Gly	Lys	Glu	Lys	Leu	
			260					265					270			
aag	gaa	ata	aaa	ctt	ttg	gtt	tgc	aat	att	gat	gga	tgt	ctc	acc	aat	864
Lys	Glu	Ile	Lys	Leu	Leu	Val	Cys	Asn	Ile	Asp	Gly	Cys	Leu	Thr	Asn	
		275					280					285				
ggc	cac	att	tat	gta	tca	gga	gac	caa	aaa	gaa	ata	ata	tct	tat	gat	912
Gly	His	Ile	Tyr	Val	Ser	Gly	Asp	Gln	Lys	Glu	Ile	Ile	Ser	Tyr	Asp	
	290					295					300					
gta	aaa	gat	gct	att	ggg	ata	agt	tta	tta	aag	aaa	agt	ggg	att	gag	960
Val	Lys	Asp	Ala	Ile	Gly	Ile	Ser	Leu	Leu	Lys	Lys	Ser	Gly	Ile	Glu	
	305				310					315					320	
gtg	agg	cta	atc	tca	gaa	agg	gcc	tgt	tca	aag	cag	acg	ctg	tct	tct	1008
Val	Arg	Leu	Ile	Ser	Glu	Arg	Ala	Cys	Ser	Lys	Gln	Thr	Leu	Ser	Ser	
				325				330						335		
tta	aaa	ctg	gat	tgc	aaa	atg	gaa	gtc	agt	gta	tca	gac	aag	cta	gca	1056
Leu	Lys	Leu	Asp	Cys	Lys	Met	Glu	Val	Ser	Val	Ser	Asp	Lys	Leu	Ala	
			340					345					350			
gtt	gta	gat	gaa	tgg	aga	aaa	gaa	atg	ggc	ctg	tgc	tgg	aaa	gaa	gtg	1104
Val	Val	Asp	Glu	Trp	Arg	Lys	Glu	Met	Gly	Leu	Cys	Trp	Lys	Glu	Val	
		355					360					365				
gca	tat	ctt	gga	aat	gaa	gtg	tct	gat	gaa	gag	tgc	ttg	aag	aga	gtg	1152
Ala	Tyr	Leu	Gly	Asn	Glu	Val	Ser	Asp	Glu	Glu	Cys	Leu	Lys	Arg	Val	
	370					375					380					
ggc	cta	agt	ggc	gct	cct	gct	gat	gcc	tgt	tcc	tac	gcc	cag	aag	gct	1200
Gly	Leu	Ser	Gly	Ala	Pro	Ala	Asp	Ala	Cys	Ser	Tyr	Ala	Gln	Lys	Ala	
	385				390				395						400	
gtt	gga	tac	att	tgc	aaa	tgt	aat	ggg	ggc	cgt	ggg	gcc	atc	cga	gaa	1248
Val	Gly	Tyr	Ile	Cys	Lys	Cys	Asn	Gly	Gly	Arg	Gly	Ala	Ile	Arg	Glu	
				405				410					415			
ttt	gca	gag	cac	att	tgc	cta	cta	atg	gaa	aaa	gtt	aat	aat	tca	tgc	1296
Phe	Ala	Glu	His	Ile	Cys	Leu	Leu	Met	Glu	Lys	Val	Asn	Asn	Ser	Cys	
			420					425					430			
caa	aaa	tag														1305

Gln Lys

<210> 4
<211> 434
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (133)..(133)
<223> The 'Xaa' at location 133 stands for His, or Tyr.

<220>
<221> misc_feature
<222> (136)..(136)
<223> The 'Xaa' at location 136 stands for Gly, or Val.

<220>
<221> misc_feature
<222> (147)..(147)
<223> The 'Xaa' at location 147 stands for Pro, or Ser.

<220>
<221> misc_feature
<222> (169)..(169)
<223> The 'Xaa' at location 169 stands for Gly, or Val.

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Gly Gly Gln Gly Arg Gly Val Glu Lys Pro Pro His Leu Ala Ala Leu
35 40 45
Ile Leu Ala Arg Gly Gly Ser Lys Gly Ile Pro Leu Lys Asn Ile Lys
50 55 60
His Leu Ala Gly Val Pro Leu Ile Gly Trp Val Leu Arg Ala Ala Leu
65 70 75 80
Asp Ser Gly Ala Phe Gln Ser Val Trp Val Ser Thr Asp His Asp Glu
85 90 95
Ile Glu Asn Val Ala Lys Gln Phe Gly Ala Gln Val His Arg Arg Ser
100 105 110
Ser Glu Val Ser Lys Asp Ser Ser Thr Ser Leu Asp Ala Ile Ile Glu
115 120 125
Phe Leu Asn Tyr Xaa Asn Glu Xaa Asp Ile Val Gly Asn Ile Gln Ala
130 135 140
Thr Ser Xaa Cys Leu His Pro Thr Asp Leu Gln Lys Val Ala Glu Met
145 150 155 160
Ile Arg Glu Glu Gly Tyr Asp Ser Xaa Phe Ser Val Val Arg Arg His
165 170 175
Gln Phe Arg Trp Ser Glu Ile Gln Lys Gly Val Arg Glu Val Thr Glu
180 185 190
Pro Leu Asn Leu Asn Pro Ala Lys Arg Pro Arg Arg Gln Asp Trp Asp
195 200 205
Gly Glu Leu Tyr Glu Asn Gly Ser Phe Tyr Phe Ala Lys Arg His Leu
210 215 220
Ile Glu Met Gly Tyr Leu Gln Gly Gly Lys Trp His Thr Thr Lys Cys
225 230 235 240
Glu Leu Glu His Ser Val Asp Ile Asp Val Asp Ile Asp Trp Pro Ile

gag ctg cag agg tac gcc gag gag gtt ggg atc ttc ttc act gcc tct	336
Glu Leu Gln Arg Tyr Ala Glu Glu Val Gly Ile Phe Phe Thr Ala Ser	
100 105 110	
ggc atg gat gag atg gca gtt gaa ttc ctg cat gaa ctg aat gtt cca	384
Gly Met Asp Glu Met Ala Val Glu Phe Leu His Glu Leu Asn Val Pro	
115 120 125	
ttt ttc aaa gtt gga tct gga gac act aat aat ttt cct tat ctg gaa	432
Phe Phe Lys Val Gly Ser Gly Asp Thr Asn Asn Phe Pro Tyr Leu Glu	
130 135 140	
aag aca gcc aaa aaa ggt cgc cca atg gtg atc tcc agt ggg atg cag	480
Lys Thr Ala Lys Lys Gly Arg Pro Met Val Ile Ser Ser Gly Met Gln	
145 150 155 160	
tca atg gac acc atg aag caa gtt tat cag atc gtg aag ccc ctc aac	528
Ser Met Asp Thr Met Lys Gln Val Tyr Gln Ile Val Lys Pro Leu Asn	
165 170 175	
ccc aac ttc tgc ttc ttg cag tgt acc agc gca tac ccg ctc cag cct	576
Pro Asn Phe Cys Phe Leu Gln Cys Thr Ser Ala Tyr Pro Leu Gln Pro	
180 185 190	
gag gac gtc aac ctg cgg gtc atc tcg gaa tat cag aag ctc ttt cct	624
Glu Asp Val Asn Leu Arg Val Ile Ser Glu Tyr Gln Lys Leu Phe Pro	
195 200 205	
gac att ccc ata ggg tat tct ggg cat gaa aca ggc ata gcg ata tct	672
Asp Ile Pro Ile Gly Tyr Ser Gly His Glu Thr Gly Ile Ala Ile Ser	
210 215 220	
gtg gcc gca gtg gct ctg ggg gcc aag gtg ttg gaa cgt cac ata act	720
Val Ala Ala Val Ala Leu Gly Ala Lys Val Leu Glu Arg His Ile Thr	
225 230 235 240	
ttg gac aag acc tgg aag ggg agt gac cac tcg gcc tcg ctg gag cct	768
Leu Asp Lys Thr Trp Lys Gly Ser Asp His Ser Ala Ser Leu Glu Pro	
245 250 255	
gga gaa ctg gcc gag ctg gtg cgg tca gtg cgt ctt gtg gag cgt gcc	816
Gly Glu Leu Ala Glu Leu Val Arg Ser Val Arg Leu Val Glu Arg Ala	
260 265 270	
ctg ggc tcc cca acc aag cag ctg ctg ccc tgt gag atg gcc tgc aat	864
Leu Gly Ser Pro Thr Lys Gln Leu Leu Pro Cys Glu Met Ala Cys Asn	
275 280 285	
gag aag ctg ggc aag tct gtg gtg gcc aaa gtg aaa att ccg gaa ggc	912
Glu Lys Leu Gly Lys Ser Val Val Ala Lys Val Lys Ile Pro Glu Gly	
290 295 300	
acc att cta aca atg gac atg ctc acc gtg aag gtg ggt gag ccc aaa	960
Thr Ile Leu Thr Met Asp Met Leu Thr Val Lys Val Gly Glu Pro Lys	
305 310 315 320	
gcc tat cct cct gaa gac atc ttt aat cta gtg ggc aag aag gtc ctg	1008
Ala Tyr Pro Pro Glu Asp Ile Phe Asn Leu Val Gly Lys Lys Val Leu	
325 330 335	

gtc act gtt gaa gag gat gac acc atc atg gaa gaa ttg gta gat aat 1056
 Val Thr Val Glu Glu Asp Asp Thr Ile Met Glu Glu Leu Val Asp Asn
 340 345 350

cat ggc aaa aaa atc aag tct taa 1080
 His Gly Lys Lys Ile Lys Ser
 355

<210> 6
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Asp Cys Ala Lys Phe Gln Lys Ser Glu Leu Glu Phe Lys Phe Asn Arg
 50 55 60
 Lys Ala Leu Glu Arg Pro Tyr Thr Ser Lys His Ser Trp Gly Lys Thr
 65 70 75 80
 Tyr Gly Glu His Lys Arg His Leu Glu Phe Ser His Asp Gln Tyr Arg
 85 90 95
 Glu Leu Gln Arg Tyr Ala Glu Glu Val Gly Ile Phe Phe Thr Ala Ser
 100 105 110
 Gly Met Asp Glu Met Ala Val Glu Phe Leu His Glu Leu Asn Val Pro
 115 120 125
 Phe Phe Lys Val Gly Ser Gly Asp Thr Asn Asn Phe Pro Tyr Leu Glu
 130 135 140
 Lys Thr Ala Lys Lys Gly Arg Pro Met Val Ile Ser Ser Gly Met Gln
 145 150 155 160
 Ser Met Asp Thr Met Lys Gln Val Tyr Gln Ile Val Lys Pro Leu Asn
 165 170 175
 Pro Asn Phe Cys Phe Leu Gln Cys Thr Ser Ala Tyr Pro Leu Gln Pro
 180 185 190
 Glu Asp Val Asn Leu Arg Val Ile Ser Glu Tyr Gln Lys Leu Phe Pro
 195 200 205
 Asp Ile Pro Ile Gly Tyr Ser Gly His Glu Thr Gly Ile Ala Ile Ser
 210 215 220
 Val Ala Ala Val Ala Leu Gly Ala Lys Val Leu Glu Arg His Ile Thr
 225 230 235 240
 Leu Asp Lys Thr Trp Lys Gly Ser Asp His Ser Ala Ser Leu Glu Pro
 245 250 255
 Gly Glu Leu Ala Glu Leu Val Arg Ser Val Arg Leu Val Glu Arg Ala
 260 265 270
 Leu Gly Ser Pro Thr Lys Gln Leu Leu Pro Cys Glu Met Ala Cys Asn
 275 280 285
 Glu Lys Leu Gly Lys Ser Val Val Ala Lys Val Lys Ile Pro Glu Gly
 290 295 300
 Thr Ile Leu Thr Met Asp Met Leu Thr Val Lys Val Gly Glu Pro Lys
 305 310 315 320
 Ala Tyr Pro Pro Glu Asp Ile Phe Asn Leu Val Gly Lys Lys Val Leu
 325 330 335
 Val Thr Val Glu Glu Asp Asp Thr Ile Met Glu Glu Leu Val Asp Asn
 340 345 350

His Gly Lys Lys Ile Lys Ser
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<210> 7
<211> 1059
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1041)

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agt gtt gat att gca aga gaa atg ata tta aaa gcc aaa gag gcc ggt 96
Ser Val Asp Ile Ala Arg Glu Met Ile Leu Lys Ala Lys Glu Ala Gly
20 25 30
gtt aat gca gta aaa ttc caa aca ttt aaa gct gat aaa tta att tca 144
Val Asn Ala Val Lys Phe Gln Thr Phe Lys Ala Asp Lys Leu Ile Ser
35 40 45
gct att gca cct aag gca gag tat caa ata aaa aac aca gga gaa tta 192
Ala Ile Ala Pro Lys Ala Glu Tyr Gln Ile Lys Asn Thr Gly Glu Leu
50 55 60
gaa tct cag tta gaa atg aca aaa aag ctt gaa atg aag tat gac gat 240
Glu Ser Gln Leu Glu Met Thr Lys Lys Leu Glu Met Lys Tyr Asp Asp
65 70 75 80
tat ctc cat cta atg gaa tat gca gtc agt tta aat tta gat gtt ttt 288
Tyr Leu His Leu Met Glu Tyr Ala Val Ser Leu Asn Leu Asp Val Phe
85 90 95
tct acc cct ttt gac gaa gac tct att gat ttt tta gca tct ttg aaa 336
Ser Thr Pro Phe Asp Glu Asp Ser Ile Asp Phe Leu Ala Ser Leu Lys
100 105 110
caa aaa ata tgg aaa atc cct tca ggt gag tta ttg aat tta ccg tat 384
Gln Lys Ile Trp Lys Ile Pro Ser Gly Glu Leu Leu Asn Leu Pro Tyr
115 120 125
ctt gaa aaa ata gcc aag ctt ccg atc cct gat aag aaa ata atc ata 432
Leu Glu Lys Ile Ala Lys Leu Pro Ile Pro Asp Lys Lys Ile Ile Ile
130 135 140
tca aca gga atg gct act att gat gag ata aaa cag tct gtt tct att 480
Ser Thr Gly Met Ala Thr Ile Asp Glu Ile Lys Gln Ser Val Ser Ile
145 150 155 160
ttt ata aat aat aaa gtt ccg gtt ggt aat att aca ata tta cat tgc 528
Phe Ile Asn Asn Lys Val Pro Val Gly Asn Ile Thr Ile Leu His Cys
165 170 175
aat act gaa tat cca acg ccc ttt gag gat gta aac ctt aat gct att 576
Asn Thr Glu Tyr Pro Thr Pro Phe Glu Asp Val Asn Leu Asn Ala Ile
180 185 190

aat gat ttg aaa aaa cac ttc cct aag aat aac ata ggc ttc tct gat 624
 Asn Asp Leu Lys Lys His Phe Pro Lys Asn Asn Ile Gly Phe Ser Asp
 195 200 205
 cat tct agc ggg ttt tat gca gct att gcg gcg gtg cct tat gga ata 672
 His Ser Ser Gly Phe Tyr Ala Ala Ile Ala Ala Val Pro Tyr Gly Ile
 210 215 220
 act ttt att gaa aaa cat ttc act tta gat aaa tct atg tct ggc cca 720
 Thr Phe Ile Glu Lys His Phe Thr Leu Asp Lys Ser Met Ser Gly Pro
 225 230 235 240
 gat cat ttg gcc tca ata gaa cct gat gaa ctg aaa cat ctt tgt att 768
 Asp His Leu Ala Ser Ile Glu Pro Asp Glu Leu Lys His Leu Cys Ile
 245 250 255
 ggg gtc agg tgt gtt gaa aaa tct tta ggt tca aat agt aaa gtg gtt 816
 Gly Val Arg Cys Val Glu Lys Ser Leu Gly Ser Asn Ser Lys Val Val
 260 265 270
 aca gct tca gaa agg aag aat aaa atc gta gca aga aag tct att ata 864
 Thr Ala Ser Glu Arg Lys Asn Lys Ile Val Ala Arg Lys Ser Ile Ile
 275 280 285
 gct aaa aca gag ata aaa aaa ggt gag gtt ttt tca gaa aaa aat ata 912
 Ala Lys Thr Glu Ile Lys Lys Gly Glu Val Phe Ser Glu Lys Asn Ile
 290 295 300
 aca aca aaa aga cct ggt aat ggt atc agt ccg atg gag tgg tat aat 960
 Thr Thr Lys Arg Pro Gly Asn Gly Ile Ser Pro Met Glu Trp Tyr Asn
 305 310 315 320
 tta ttg ggt aaa att gca gag caa gac ttt att cca gat gaa tta ata 1008
 Leu Leu Gly Lys Ile Ala Glu Gln Asp Phe Ile Pro Asp Glu Leu Ile
 325 330 335
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 Ile His Ser Glu Phe Lys Asn Gln Gly Glu
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 Val Asn Ala Val Lys Phe Gln Thr Phe Lys Ala Asp Lys Leu Ile Ser
 35 40 45
 Ala Ile Ala Pro Lys Ala Glu Tyr Gln Ile Lys Asn Thr Gly Glu Leu
 50 55 60
 Glu Ser Gln Leu Glu Met Thr Lys Lys Leu Glu Met Lys Tyr Asp Asp
 65 70 75 80
 Tyr Leu His Leu Met Glu Tyr Ala Val Ser Leu Asn Leu Asp Val Phe
 85 90 95

Ser	Thr	Pro	Phe	Asp	Glu	Asp	Ser	Ile	Asp	Phe	Leu	Ala	Ser	Leu	Lys
			100					105					110		
Gln	Lys	Ile	Trp	Lys	Ile	Pro	Ser	Gly	Glu	Leu	Leu	Asn	Leu	Pro	Tyr
		115					120					125			
Leu	Glu	Lys	Ile	Ala	Lys	Leu	Pro	Ile	Pro	Asp	Lys	Lys	Ile	Ile	Ile
	130					135					140				
Ser	Thr	Gly	Met	Ala	Thr	Ile	Asp	Glu	Ile	Lys	Gln	Ser	Val	Ser	Ile
145					150					155					160
Phe	Ile	Asn	Asn	Lys	Val	Pro	Val	Gly	Asn	Ile	Thr	Ile	Leu	His	Cys
			165						170					175	
Asn	Thr	Glu	Tyr	Pro	Thr	Pro	Phe	Glu	Asp	Val	Asn	Leu	Asn	Ala	Ile
		180						185				190			
Asn	Asp	Leu	Lys	Lys	His	Phe	Pro	Lys	Asn	Asn	Ile	Gly	Phe	Ser	Asp
		195					200					205			
His	Ser	Ser	Gly	Phe	Tyr	Ala	Ala	Ile	Ala	Ala	Val	Pro	Tyr	Gly	Ile
	210					215					220				
Thr	Phe	Ile	Glu	Lys	His	Phe	Thr	Leu	Asp	Lys	Ser	Met	Ser	Gly	Pro
225					230					235					240
Asp	His	Leu	Ala	Ser	Ile	Glu	Pro	Asp	Glu	Leu	Lys	His	Leu	Cys	Ile
			245						250					255	
Gly	Val	Arg	Cys	Val	Glu	Lys	Ser	Leu	Gly	Ser	Asn	Ser	Lys	Val	Val
		260						265					270		
Thr	Ala	Ser	Glu	Arg	Lys	Asn	Lys	Ile	Val	Ala	Arg	Lys	Ser	Ile	Ile
		275					280					285			
Ala	Lys	Thr	Glu	Ile	Lys	Lys	Gly	Glu	Val	Phe	Ser	Glu	Lys	Asn	Ile
	290					295					300				
Thr	Thr	Lys	Arg	Pro	Gly	Asn	Gly	Ile	Ser	Pro	Met	Glu	Trp	Tyr	Asn
305					310					315					320
Leu	Leu	Gly	Lys	Ile	Ala	Glu	Gln	Asp	Phe	Ile	Pro	Asp	Glu	Leu	Ile
			325						330					335	
Ile	His	Ser	Glu	Phe	Lys	Asn	Gln	Gly	Glu						
			340					345							

*BI
concluded*